Research Article

Genome Mining Reveals Plant Growth-Promoting and Antagonistic Potential of *Streptomyces* sp. S.PB5 Obtained from an Extinct Volcanic Soil

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Abstract | *Streptomyces* species are increasingly recognized as multifunctional plant growth-promoting bacteria with potential applications in sustainable agriculture. This study aimed to investigate the genomic basis of plant growth-promoting and antagonistic traits in a genomically distinct *Streptomyces* isolate (S.PB5) recovered from a cultivated soil associated with extinct volcanic area in northeastern Thailand through an integrated genome mining and structural modelling approach. Whole-genome sequencing and annotation were performed using the NCBI Prokaryotic Genome Annotation Pipeline, followed by functional annotation using BV-BRC and the RAST/SEED framework. Phylogenomic analysis based on average nucleotide identity and digital DNA–DNA hybridization demonstrated that strain S.PB5 represents a distinct genomic lineage within the genus *Streptomyces*. The draft genome (10.85 Mb; 70.57% GC content) encoded 9,485 protein-coding genes and harbored diverse biosynthetic gene clusters associated with ectoine, terpenes, siderophores, ribosomally synthesized peptides, and polyketide pathways. In silico structural analysis revealed conserved catalytic folds and domain organization among the selected biosynthetic enzymes, supporting the predicted biosynthetic functions. The genomic features identified in S.PB5 are consistent with broad metabolic versatility, ecological adaptability, and previously reported plant-associated phenotypes. Collectively, the findings demonstrate that volcanic-associated soils may serve as reservoirs of genomically distinct and functionally diverse *Streptomyces* strains and highlight the value of integrating genome mining with structural modelling to predict traits relevant to sustainable agriculture and microbial biotechnology.

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Introduction

Sustained agricultural productivity depends not only on crop genetics and agronomic inputs but also on biological condition of the soils. Soil ecosystems support nutrient cycling, organic matter turnover, and plant health through complex microbial communities that interact continuously with the plant roots (Liang *et al*., 2015; Lambers and Wen-Feng, 2022). However, intensive agricultural practices are increasingly associated with soil degradation, including reductions in organic matter, nutrient imbalances, and declining microbial diversity. These changes can impair soil ecosystem functions and increase the vulnerability of agroecosystems to both biotic and abiotic stress.

Environmental stresses and conventional agricultural inputs further contribute to the deterioration of soil health. Drought and soil salinity have been shown to alter soil microbial community structure and function, disrupt plant–microbe interactions, and ultimately reduce crop productivity (Shrivastava and Kumar, 2015; De Silva *et al*., 2025). In addition, although mineral fertilizers and chemical pesticides have contributed substantially to crop yield improvement, their prolonged use may negatively affect the beneficial soil microorganisms and promote the emergence of resistant pathogens (Santos *et al*., 2012; Gangwar *et al*., 2018; Pathak *et al*., 2022; Pandey and Saharan, 2025). These concerns have stimulated increasing interest in sustainable biological alternatives capable of enhancing crop performance while maintaining soil ecological integrity.

The use of plant growth-promoting bacteria (PGPB) has attracted increasing attention in sustainable crop management systems because they can enhance plant performance through several mechanisms, including nutrient mobilization, phytohormone production, stress modification, and interactions with soil-borne pathogens (Scarano *et al*., 2020; Bouremani *et al*., 2023; Górska *et al*., 2024; Lü *et al*., 2024). In addition, PGPB can influence soil structure and microbial community stability; thereby, contributing to long-term soil resilience (Hassan *et al*., 2019; Sharma *et al*., 2021; Pérez-Montaño *et al*., 2025). The effectiveness of these microorganisms depends not only on their metabolic traits but also on their ability to establish and persist in the rhizosphere.

Several bacterial genera, including *Pseudomonas*, *Bacillus*, *Azospirillum*, *Azotobacter*, and *Streptomyces*, have been investigated as plant growth–promoting bacteria, and some have been developed for agricultural applications (Franco-Correa *et al*., 2010; Ahmed and Holmström, 2014; Baba *et al*., 2015; Saha *et al*., 2016; Lopes *et al*., 2021). Within this group, the genus *Streptomyces* (phylum Actinobacteria) is recognized for its adaptive metabolism, extensive secondary metabolite biosynthesis, and ability to establish persistent interactions within the rhizosphere environments. Members of this genus exhibit filamentous growth, produce resistant spores, and possess large, GC-rich genomes that encode extensive metabolic and regulatory capacity (Hopwood, 2019; Khadayat *et al*., 2020; Lee *et al*., 2020). These characteristics are associated with persistence under nutrient limitation, water stress, and other adverse soil conditions. In addition to their ecological adaptability, *Streptomyces* species are well known for producing a wide range of secondary metabolites, including antibiotics and other bioactive compounds that can inhibit plant pathogens (Amaresan *et al*., 2018; Kontro *et al*., 2022). Many strains have also been reported to support plant growth through multiple mechanisms such as auxin production, phosphate solubilization, and secretion of extracellular enzymes that influence nutrient availability in the soil (Feikema and Baker, 2011; Sadeghi *et al*., 2012; Talebi Atouei *et al*., 2019). Some isolates have been shown to affect plant stress responses and defense pathways, although the magnitude and consistency of these effects vary among the strains and the environmental contexts (Viaene *et al*., 2016; Singh and Gaur, 2017; Myo *et al*., 2019). Despite this growing body of evidence, the functional diversity of *Streptomyces* populations in agricultural soils, particularly in distinctive or underexplored environments, remains only partially characterized.

Recent advances in genome sequencing and genome mining have made it possible to investigate the genetic basis underlying the multifunctional traits of actinobacteria. Whole-genome analyses have revealed that *Streptomyces* genomes typically contain large numbers of biosynthetic gene clusters, as along with genes associated with phytohormone biosynthesis, nutrient acquisition, stress tolerance, and antimicrobial compound production (Ashraf *et al*., 2022; Pengproh *et al*., 2023). Such genomic information provides a framework for linking observed phenotypes to underlying metabolic potential and supports

the targeted selection of strains for agricultural applications. In an earlier work, *Streptomyces* sp. isolate S.PB5 was recovered from cultivated soils in extinct volcanic areas of northeastern Thailand and shown to exhibit plant growth–promoting and antagonistic properties (Pengproh *et al*., 2023). This isolate displayed consistent inhibitory activity against *Fusarium oxysporum* f. sp. *lycopersici*, associated with the production of extracellular hydrolytic enzymes such as amylase and cellulase. Microscopic observations indicated that fungal hyphae exposed to metabolites from the isolate S.PB5 developed abnormal morphology and cytoplasmic disorganization, suggesting an antibiosis-related interaction. In addition, isolate S.PB5 produced indole-3-acetic acid, solubilized phosphate, and enhanced tomato seedling growth and biomass accumulation under pot conditions.

Given the increasing pressures originating from soil degradation, climate variability, and reduced reliance on chemical inputs, further evaluation of *Streptomyces*-based PGPB is warranted. Although numerous *Streptomyces* species have been reported to possess plant growth-promoting and antagonistic activities, genome-informed characterization of the isolates originating from volcanic-associated soils remains limited. In particular, the integration of phylogenomic analysis, genome mining, and structural modelling to evaluate the multifunctional traits of volcanic-associated *Streptomyces* isolates has rarely been explored. Therefore, the present study aimed to characterize the genome of *Streptomyces* sp. S.PB5, a strain isolated from a cultivated soil associated with extinct volcanic areas in northeastern Thailand, using a whole-genome sequencing, genome mining, and structural modelling approaches. The study sought to identify genetic determinants associated with plant growth promotion and antagonism and provide a genomic framework for evaluating *Streptomyces* sp. S.PB5 potential as a bio-inoculant for sustainable agriculture.

Materials and Methods

Isolation and cultivation of Streptomyces sp. isolate S.PB5

Streptomyces sp. S.PB5 was previously isolated from a cultivated soil near the extinct Plai Bud volcano in Chorakhe Mak Subdistrict, Prakhon Chai District, Buriram Province, Thailand (14.4813066° N, 102.9683925° E) and was phenotypically characterized for plant growth-promoting and antagonistic traits by Pengproh *et al*. (2023). The soil sample was collected from an organic farming area located adjacent to the volcanic site. The soil was characterized as clayey soil with a compact structure, dark gray to black coloration, and an average pH of 8. In the present study, this previously characterized isolate was used for whole-genome sequencing and genome mining. Briefly, the original isolation followed a modified method described by Kawicha *et al*. (2020), using arginine–glycerol mineral salt agar (AGMA) for the selective isolation of *Streptomyces*-like colonies. Purified cultures were maintained on half-strength potato dextrose agar (HPDA) slants at 4°C until further analysis. The taxonomic placement of isolate S.PB5 was further confirmed in this study using whole-genome-based analyses, including TYGS [Type (Strain) Genome Server], ANI (average nucleotide identity), and dDDH (digital DNA–DNA hybridization) comparisons.

Genomic DNA extraction and quality assessment

Genomic DNA was extracted from freshly grown cultures of *Streptomyces* sp. isolate S.PB5 cultivated in HPDB medium at 37 °C for seven d. The cells were harvested and homogenized in liquid nitrogen according to the method described by Pengproh *et al*. (2023) prior to genomic DNA extraction using the GeneJET Genomic DNA Purification Kit (Thermo Fisher Scientific, USA), following the manufacturer's instructions for Gram-positive bacteria. DNA concentration and purity were assessed spectrophotometrically using a NanoDrop spectrophotometer (NanoDrop Lite, Thermo Fisher Scientific, the United States), while DNA integrity was evaluated by electrophoresis on a 1% agarose gel. Intact high-molecular-weight genomic DNA without visible smearing was observed prior to sequencing.

Whole-genome sequencing and phylogenetic analysis

Purified genomic DNA was submitted to Macrogen Inc. (Seoul, Republic of Korea) for paired-end sequencing using the Illumina platform and TruSeq Nano DNA library preparation. The prepared DNA library passed quality control assessment with a concentration of 70.71 ng/µl, 184.38 nM, and an average library size of 590 bp. A total of 8,428,740 raw reads comprising 851,302,740 bases were generated, with Q20 and Q30 values of 96.02% and 93.01%, respectively. After quality filtering using Trimmomatic, 6,918,832 reads comprising 698,094,807 bases were retained

for *de novo* assembly using SPAdes version 3.13.0. The final assembly had an estimated sequencing depth of approximately 64X. Assembly quality was evaluated based on sequencing depth, self-mapping statistics, and BUSCO completeness analysis using the bacteria_odb10 lineage dataset. The draft genome sequence of *Streptomyces* sp. S.PB5 has been deposited in GenBank under the Whole Genome Shotgun (WGS) accession number: JAQMWP000000000. The taxonomic and phylogenetic placement of isolate S.PB5 was determined using the Type (Strain) Genome Server (TYGS) (Meier-Kolthoff and Göker, 2019). Genome relatedness was further evaluated by calculating the Average Nucleotide Identity based on BLAST (ANIb) and MUMmer (ANIm) using the JSpeciesWS platform (Richter *et al*., 2016), while digital DNA–DNA hybridization (dDDH) values (formula d4) were obtained directly from TYGS. Species-level assignments were determined according to the widely accepted thresholds of ≥95–96% for ANI and ≥70% for dDDH.

Genome annotation

The assembled genome of *Streptomyces* sp. S.PB5 was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (Tatusova *et al*., 2016) to predict the protein-coding sequences and RNA genes. Subsystem-based functional annotation was subsequently performed using the BV-BRC (formerly PATRIC) platform (Wattam *et al*., 2017; Olson *et al*., 2023), which classified the predicted genes into curated functional subsystems based on the comparative genomics and the expert annotation frameworks. The resulting subsystem assignments were used to generate an overview of the functional composition of the genome.

Prediction of biosynthetic gene clusters and genes associated with plant growth–promoting and antagonistic traits

Biosynthetic gene clusters (BGCs) associated with secondary metabolite production were predicted using antiSMASH version 8.0.1 (Blin *et al*., 2025) with relaxed detection settings. Identified BGCs were annotated through comparison with the Minimum Information about a Biosynthetic Gene cluster (MIBiG) database and only clusters showing ≥70% similarity to the characterized reference BGCs were considered for further analysis.

In addition, genes associated with the plant growth–promoting and the antagonistic traits were identified based on the functional annotation using the Rapid Annotation using Subsystems Technology (RAST) platform, which assigned the predicted genes to functional categories according to the SEED Subsystems framework (Overbeek *et al*., 2014).

Homology modelling and structural annotation

Six representative proteins were selected from high-confidence biosynthetic gene clusters based on the confidence of the functional annotation, their predicted roles as key catalytic enzymes within each pathway, and the availability of suitable structural templates. The selected proteins included IucA/IucC family siderophore biosynthesis protein, lysine N6-monooxygenase, type I polyketide synthase-like protein, polyprenyl synthase family protein, squalene–hopene cyclase, and type III polyketide synthase. These proteins were selected as representative enzymes of siderophore-, terpene-, and polyketide-associated biosynthetic pathways identified in the genome.

Amino acid sequences were analyzed using the SWISS-MODEL server for an automated comparative modelling (Bienert *et al*., 2017; Waterhouse *et al*., 2018). Template identification was conducted using the BLAST (Camacho *et al*., 2009) and the HHblits (Steinegger *et al*., 2019) searches against the SWISS-MODEL Template Library, which integrates the experimentally resolved structures from the Protein Data Bank. Model reliability was assessed using the Global Model Quality Estimation (GMQE) and the QMEAN metrics (Studer *et al*., 2020, 2021). Structural interpretation focused on conserved catalytic folds, domain organization, and topology similarity between the predicted proteins and the experimentally characterized biosynthetic enzymes. Structural interpretations were applied conservatively to support the predicted biosynthetic functions without directly inferring the enzymatic activity, pathway completeness, or the confirmed metabolite production (Medema and Fischbach, 2015).

Results

Whole-genome features of Streptomyces sp. S.PB5

Whole-genome sequencing of *Streptomyces* sp. S.PB5 generated a draft genome assembly with a total size of 10,853,119 bp and a GC content of 70.57%, assembled into 67 contigs. The assembly showed a N50 value of 501,857 bp, with the longest contig reaching 1,081,601 bp. Sequencing

depth was estimated at approximately 64×, while self-mapping analysis demonstrated 99.92% read mapping and 100% genome coverage. Genome completeness assessment using BUSCO identified 99.19% complete BUSCOs based on the bacteria_odb10 lineage dataset, indicating a highly complete assembly (Table 1). Genome annotation using the NCBI Prokaryotic Genome Annotation Pipeline predicted 9,485 protein-coding genes and 90 RNA genes, including multiple rRNA and tRNA copies. The relatively large genome size, high GC content, and extensive coding capacity are consistent with the metabolic versatility and ecological adaptability commonly reported in the soil-associated *Streptomyces* species. In addition, the abundance of genes associated with metabolism, regulation, transport systems, and secondary metabolite biosynthesis suggests a broad functional potential that may contribute to environmental persistence, microbial competition, and plant-associated interactions in the soil ecosystems. Visualization of genome annotations using BV-BRC revealed the distribution of coding sequences, RNA genes, antimicrobial resistance–related genes, virulence factor homologs, GC content, and GC skew across the genome (Figure 1), providing an overview of the genomic organization of *Streptomyces* isolate S.PB5.

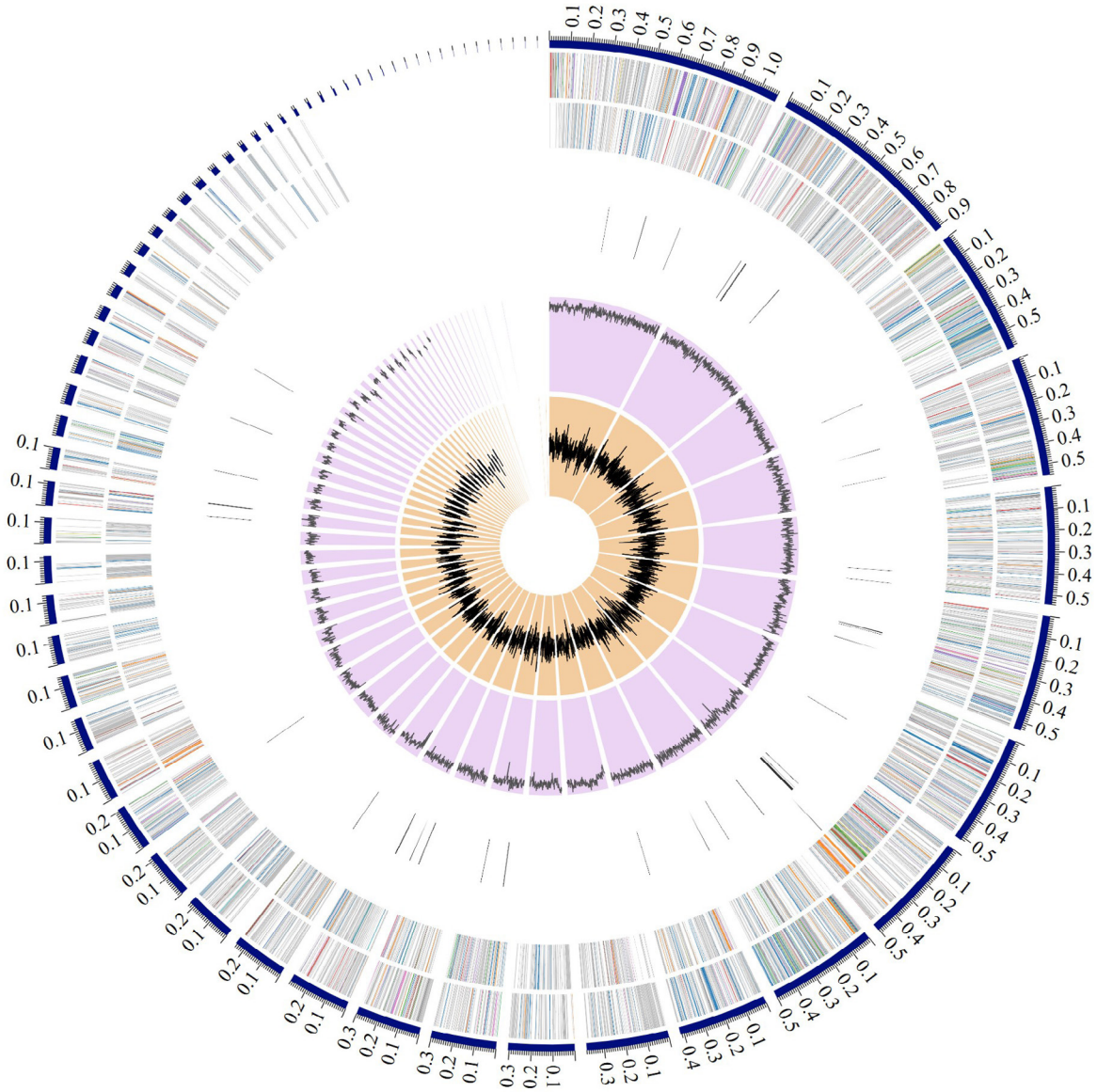

Figure 1: *Circular genome map of Streptomyces sp. S.PB5 generated using BV-BRC (PATRIC). The circular representation shows, from the outermost to the innermost rings, contigs, coding sequences (CDSs) on the forward strand, CDSs on the reverse strand, RNA genes, CDSs with homology to antimicrobial resistance genes, CDSs with homology to virulence factors, GC content, and GC skew. CDSs on both strands are color-coded according to functional subsystems assigned by BV-BRC annotation.*

Table 1: *Genome assembly statistics of Streptomyces sp. isolate S.PB5.*

Feature	Value
Assembly method	SPAdes v3.13.0
Genome size	10,853,119 bp
Number of contigs	67
GC content	70.57%
N50	501,857 bp
Longest contig	1,081,601 bp
Sequencing depth	64X
Genome coverage	100%
Mapped reads	99.92%
Complete BUSCOs	99.19%
Fragmented BUSCOs	0%
Missing BUSCOs	0%

Phylogenomic placement based on whole-genome analysis

Whole genome based phylogenetic analysis confirmed the affiliation of isolate S.PB5 with the genus *Streptomyces*. Comparative analysis using the TYGS showed that isolate S.PB5 is most closely related to several recognized *Streptomyces* type strains but forms a distinct lineage in the genome-based phylogenetic tree (Figure 2). This topology indicates genetic relatedness to the established taxa while suggesting that isolate S.PB5 does not cluster within the boundaries of any currently described species.

To further quantify the genome-level relatedness, ANI and dDDH were calculated. The highest dDDH value obtained using the GBDP formula d4 was 33.0% against *Streptomyces aquilus* GGCR-6^{T}. Since bacterial strains belonging to the same species are generally expected to exhibit dDDH values of ≥70%, the observed value strongly supported the classification of *Streptomyces* sp. isolate S.PB5 as a distinct genomic species-level lineage (Table 2). Similarly, the highest ANI values observed were 85.67% (ANIb) and 88.69% (ANIm), both of which fell below the accepted species-level cutoff of 95–96%.

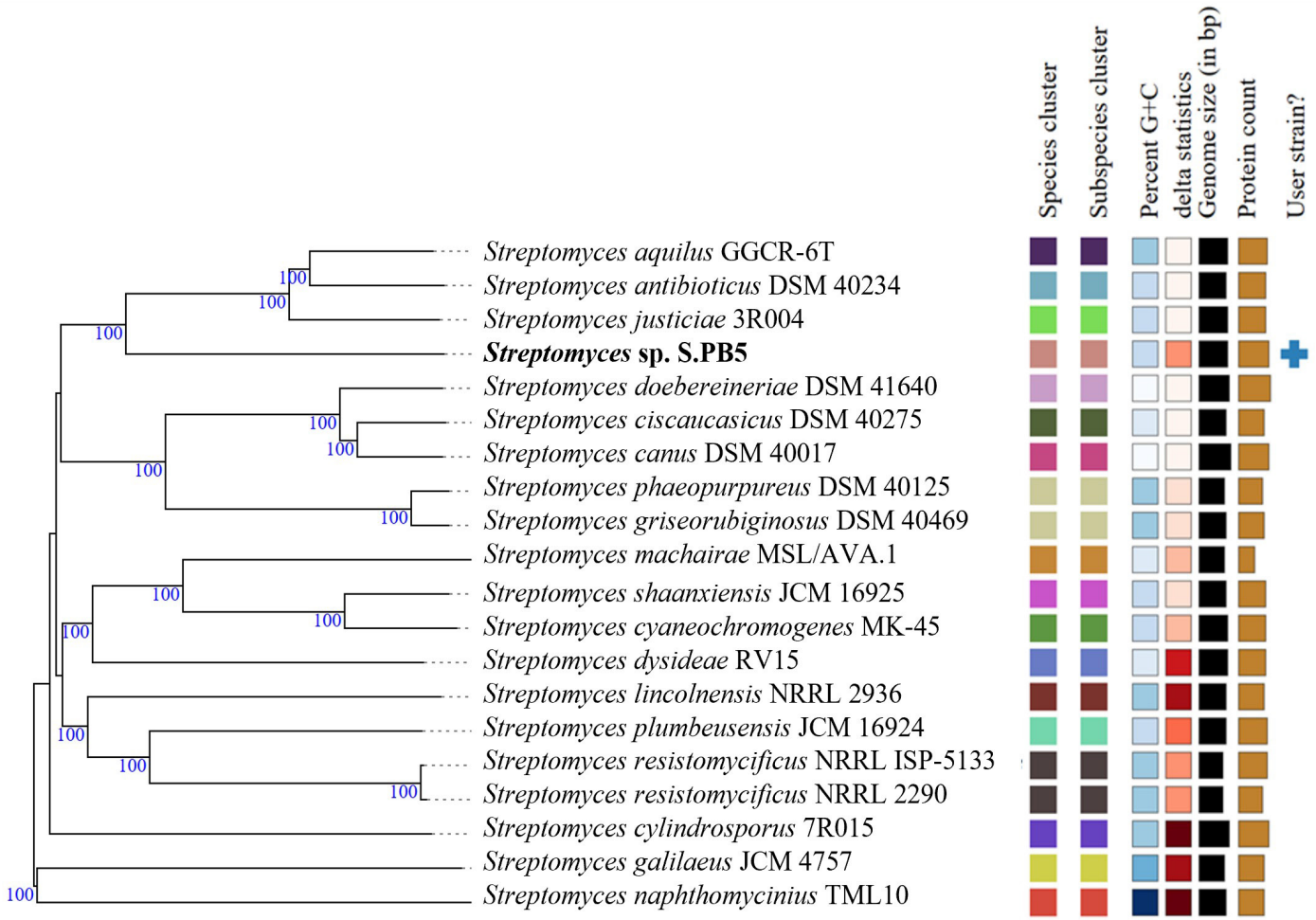

Figure 2: *Genome-based phylogenetic tree showing the placement of Streptomyces sp. S.PB5 among closely related Streptomyces type strains, reconstructed using the TYGS/GBDP approach. Bootstrap support values are indicated at the corresponding nodes.*

Taken together, the results obtained from the genome-based phylogenetic reconstruction, ANI, and dDDH analyses consistently indicate that although isolate S.PB5 was affiliated with the genus *Streptomyces*, it represented a genomically distinct taxon. Accordingly, the isolate was designated as *Streptomyces* sp. S.PB5 rather than being assigned to an existing species. This genome-based taxonomic placement provided a robust framework for subsequent analyses of the functional genes and the biosynthetic potential.

Functional annotation based on BV-BRC platforms

Subsystem-based functional annotation using the BV-BRC platform assigned the predicted genes of *Streptomyces* sp. S.PB5 to diverse functional categories associated with metabolism, environmental adaptation, and cellular regulation (Figure 3). Metabolism-related subsystems represented the largest functional category, comprising 111 subsystems and 1,158 associated genes, followed by protein processing (42 subsystems, 270 genes), stress response and defense-related functions (41 subsystems, 203 genes), and energy metabolism (33 subsystems, 420 genes). Additional functional categories included membrane transport, cellular processes, DNA and RNA processing, and regulation and cell signaling, reflecting a broad metabolic versatility and an ecological adaptability typical of the soil-associated *Streptomyces* species. The presence of genes associated with nutrient acquisition, stress adaptation, transport systems, and secondary metabolism is consistent with the previously reported plant growth–promoting and antagonistic phenotypes of isolate S.PB5, including siderophore production, phosphate solubilization, and antimicrobial activity.

Table 2: *Genome-based taxonomic relatedness between Streptomyces sp. isolate S.PB5 and the closely related type strains inferred from ANI and dDDH (formula d4).*

Subject strain (type strain)	ANIb (%)	ANIm (%)	dDDH (d4, %)
Streptomyces aquilus GGCR-6^T	85.60	88.69	33.0
Streptomyces antibiotica DSM 40234^T	85.61	88.68	32.9
Streptomyces justiciae 3R004^T	85.67	88.67	32.9
Streptomyces griseorubiginosus DSM 40469^T	82.63	87.05	28.3
Streptomyces canus DSM 40017^T	82.62	87.01	28.4
Streptomyces doebereinerae DSM 41640^T	82.61	87.00	28.4

Where; Species delineation thresholds generally correspond to 95–96% for average nucleotide identity (ANI) and 70% for digital DNA–DNA hybridization (dDDH). ANIb refers to average nucleotide identity based on BLAST, whereas ANIm refers to average nucleotide identity based on MUMmer. dDDH values are reported using Genome-to-Genome Distance Calculator (GGDC) formula d4, which is independent of genome length and recommended for draft genomes by TYGS.

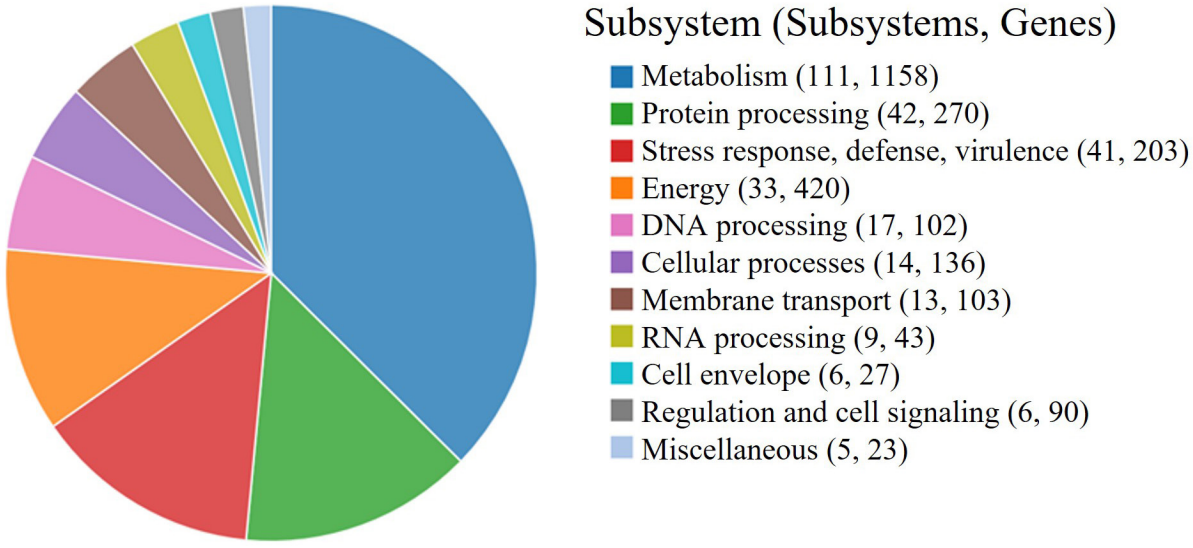

Figure 3: *Subsystem-based functional annotation of the Streptomyces sp. S.PB5 genome generated using the BV-BRC platform. The annotated genes were primarily associated with metabolism, protein processing, stress adaptation, energy production, membrane transport, and regulatory functions, reflecting the broad metabolic versatility and ecological adaptability of the isolate.*

Biosynthetic gene clusters predicted using antiSMASH

Genome mining using antiSMASH identified 13 biosynthetic gene clusters (BGCs) in the genome of *Streptomyces* sp. S.PB5, representing diverse classes of secondary metabolite pathways (Table 3, Figure 4). These BGCs included nonribosomal peptide synthetase (NRPS)-associated clusters, polyketide synthase (PKS) clusters (Type I and Type III), hybrid nonribosomal peptide synthetase–polyketide synthase (NRPS–PKS) systems, and several terpene and ribosomally synthesized and post-translationally modified peptide (RiPP)-related clusters (including lassopeptide/lanthipeptide-type regions). Several predicted BGCs showed high similarity to the characterized reference clusters in the MIBiG database, including those associated with the biosynthesis of ectoine, geosmin, ε-poly-L-lysine, coelichelin, albaflavenone, informatipeptin, and flaviolin/1,3,6,8-tetrahydroxynaphthalene (100% similarity) (Table 3). Additional clusters displayed a moderate similarity to the known pathways, such as desferrioxamine B/E (83%) and hopene (92%), whereas several regions displayed a lower similarity (<60%), suggesting potentially divergent or less well-characterized biosynthetic architectures. Overall, the diversity of the BGC classes and the presence of multiple clusters related to the bioactive and/or the iron-scavenging metabolites provide a genomic basis for the secondary metabolic potential of isolate S.PB5, in consistency with its antagonism-related phenotype observed *in vitro*.

Table 3: *Biosynthetic gene clusters predicted in Streptomyces sp. isolate S.PB5 using antiSMASH and their similarity to MIBiG reference clusters.*

Region	BGC type	Start (bp)	End (bp)	Most similar biosynthetic gene cluster	Similarity (%)
1.2	Ectoine	975,825	986,235	Ectoine	100
2.4	Terpene	508,422	530,584	Geosmin	100
3.1	NAPAA (non-α-poly-amino acid).	157,613	191,464	ε-Poly-L-lysine	100
3.2	Type I PKS (T1PKS).	236,182	279,193	4-hexadecanoyl-3-hydroxy-2-(hydroxymethyl)-2H-furan-5-one	54
4.1	NI-siderophore (NRPS-independent).	154,096	183,868	Desferrioxamine B/E	83
7.1	NRP-metallophore (NRPS–PKS hybrid)	66,032	162,138	Coelichelin	100
7.2	Melanin	442,904	453,254	Melanin	57
10.2	Terpene	203,462	230,082	Hopene	92
12.1	NRPS, lassopeptide.	1	45,737	Ullenugdin / Huascopentin	50
14.2	Terpene	181,361	202,374	Albaflavenone	100
15.1	RiPP-like lanthipeptide class III.	14,493	41,978	Informatipeptin	100
19.1	Type III PKS (T3PKS).	162,749	203,810	Flaviolin / 1,3,6,8-tetrahydroxynaphthalene	100
25.1	NRPS–T1PKS hybrid.	1	76,631	Aurantimycin A	55

Where; BGC indicates a biosynthetic gene cluster, antiSMASH indicates antibiotics and Secondary Metabolite Analysis Shell, MIBiG indicates Minimum Information about a Biosynthetic Gene Cluster, NAPAA indicates a non-α-poly-amino acid biosynthetic pathway, NRPS indicates nonribosomal peptide synthetase, PKS indicates polyketide synthase, T1PKS indicates type I polyketide synthase, T3PKS indicates type III polyketide synthase, NRPS–PKS indicates a nonribosomal peptide synthetase–polyketide synthase hybrid cluster, and RiPP indicates a ribosomally synthesized and post-translationally modified peptide.

Genes associated with predicted antibiotic and antagonistic functions

Genome annotation identified several genes associated with predicted antibiotic and antagonistic functions in the genome of *Streptomyces* sp. S.PB5 (Table 4). These genes included those encoding PKS components, enzymes involved in secondary metabolite modification, such as monooxygenases, as along with proteins associated with enediyne-type biosynthetic pathways. Additional annotated genes belonged to the protein families previously linked to secondary metabolism and bioactive compounds production. Collectively, the presence of these genes supports the genomic potential of isolate S.PB5 to produce secondary metabolites with possible antagonistic properties. However, the specific roles of these genes and their contributions to the antimicrobial activity require further experimental validation.

Table 4: *Genes associated with predicted antibiotic and antagonistic functions in Streptomyces sp. isolate S.PB5.*

Gene	Locus tag	Predicted function / product
priA	03100	Bifunctional protein involved in secondary metabolism
NA	10620	Aminodeoxychorismate lyase
NA	15050	Penicillin acylase family protein
NA	15420	Antibiotic biosynthesis monooxygenase
NA	05600	Type I polyketide synthase
NA	12835	Enediyne biosynthesis protein

Where; NA indicates that no standardized gene name is available and the gene is referred to by its locus tag.

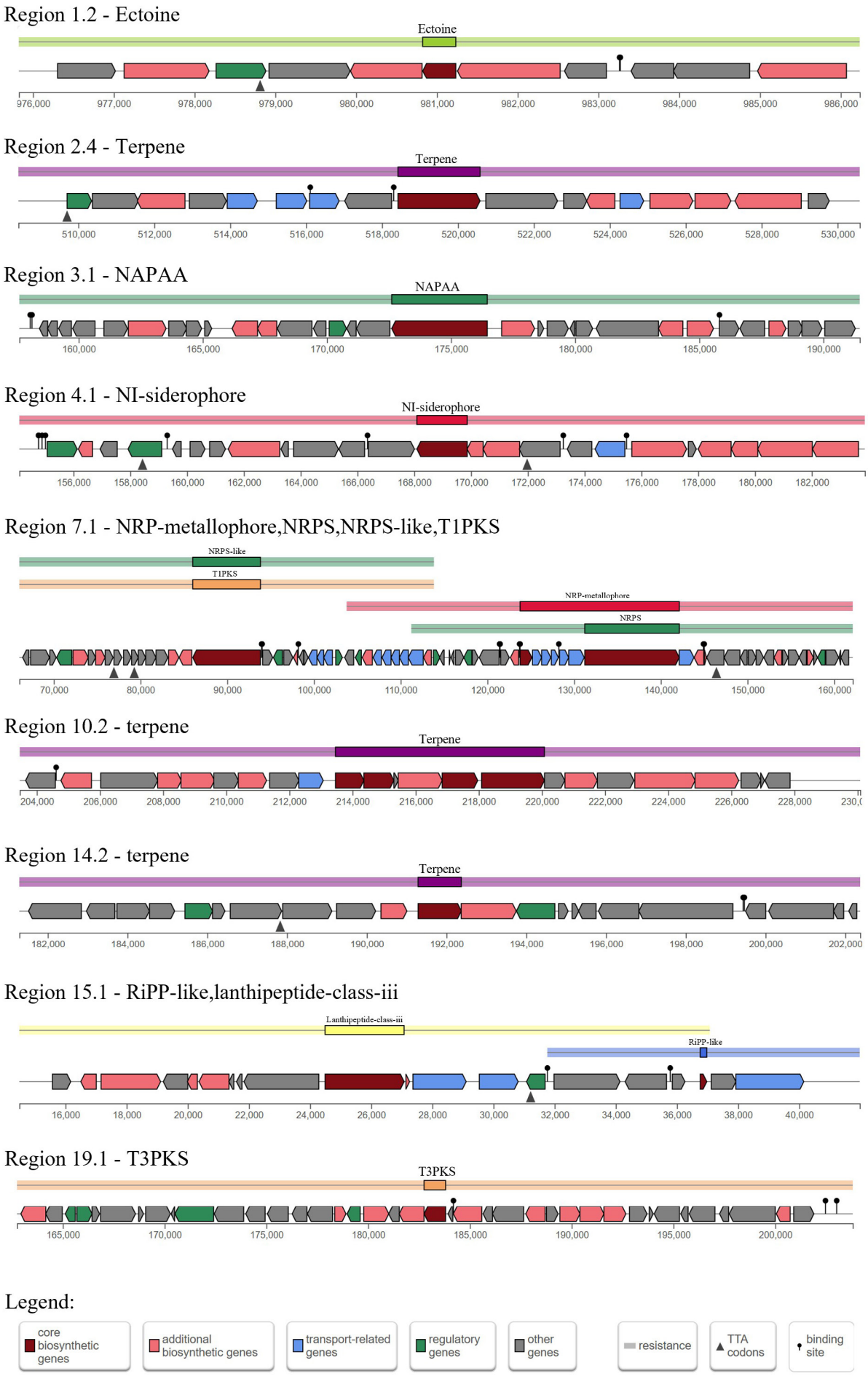

Figure 4: *Representative biosynthetic gene clusters predicted in Streptomyces sp. S.PB5 using antiSMASH.*

Genes associated with predicted plant growth–promoting traits

Genome annotation revealed multiple genes associated with predicted plant growth–promoting (PGP) traits in *Streptomyces* sp. S.PB5 (Table 5). These genes included those involved in indole-3-acetic acid (IAA)–related biosynthetic pathways, such as enzymes of the tryptophan metabolic route, as well as genes associated with siderophore biosynthesis and iron acquisition, including *iucA/iucC* family proteins and heme transport components. Additional annotated genes were linked to nitrogen metabolism and recycling, including glutamine and glutamate metabolism, urea decomposition-related enzymes, and aminotransferases. Genes associated with phosphate metabolism, such as alkaline phosphatases and inorganic phosphate transporters, were also identified. Collectively, the presence of these genes highlights the genomic potential of isolate S.PB5 to support plant growth through multiple nutrient-related and hormone-associated mechanisms, although functional validation is required to confirm their activity in planta.

Table 5: *Genes associated with predicted plant growth–promoting traits in Streptomyces sp. isolate S.PB5.*

Gene	Locus tag	Predicted function / product	Pathway
NA	06695	Indole-3-glycerol phosphate synthase.	Auxin biosynthesis
trpD	02580	Anthranilate phosphoribosyltransferase.	
trpB	03165	Tryptophan synthase subunit beta.	
trpA	03170	Tryptophan synthase subunit alpha.	
NA	07215	Monoamine oxidase (copper amine oxidase).	
NA	05185	IucA/IucC family protein.	Siderophore biosynthesis
NA	07925	IucA/IucC family siderophore biosynthesis protein.	
NA	10160, 12345	Siderophore-interacting protein.	
NA	05180	Aminotransferase class III-fold PLP-dependent enzyme.	
NA	05190	GNAT family N-acetyltransferase.	
NA	02010	NAD(+) synthase	Nitrogen metabolism
NA	02185	Glutamine synthetase beta-grasp.	
hisH	03095	Imidazole glycerol phosphate synthase subunit HisH.	
gltB	03225	Glutamate synthase large subunit.	
NA	03560	Aspartate/glutamate racemase family protein.	
metH	09835	Methionine synthase	Iron acquisition and metabolism
NA	03700	Carboxymuconolactone decarboxylase family protein.	
NA	01870	Heme ABC transporter ATP-binding protein.	
argH	10425	Argininosuccinate lyase	Urea decomposition
atzF	10070	Allophanate hydrolase	
NA	10080, 10085	Urea carboxylase-associated family protein.	
NA	11375	Allophanate hydrolase subunit 1	
mtnC	09785	Acireductone synthase	Phosphate metabolism
pdxT	10770	Pyridoxal 5′-phosphate synthase glutaminase subunit PdxT.	
NA	13725	Alkaline phosphatase D family protein.	
NA	04575	Inorganic phosphate transporter.	

Where; NA indicates that no standardized gene name is available and the gene is referred to by its locus tag.

Table 6: *Structural modelling of selected biosynthetic proteins predicted in Streptomyces sp. isolate S.PB5.*

Region	Predicted protein	Structural template	Sequence identity (%)	Structural interpretation
4.1	IucA/IucC family siderophore biosynthesis protein.	Siderophore synthetase DesD	83.36	Conserved siderophore synthetase fold associated with hydroxamate-type siderophore biosynthesis.
7.1	Type I polyketide synthase-like protein.	Rifamycin polyketide synthase	76.10	Conserved modular PKS architecture involved in polyketide chain elongation.
7.1	Lysine N6-monooxygenase.	L-lysine N6-monooxygenase MbtG	83.52	Conserved flavin-dependent monooxygenase fold involved in siderophore precursor biosynthesis.
10.2	Polyprenyl synthetase family protein.	Polyprenyl synthetase	93.55	Conserved prenyltransferase topology associated with terpene biosynthesis.
10.2	Squalene–hopene cyclase.	Squalene–hopene cyclase	92.76	Conserved cyclase fold associated with hopanoid biosynthesis.
19.1	Type III polyketide synthase.	THNS polyketide synthase	88.57	Conserved catalytic architecture characteristic of bacterial type III PKSs.

Where; IucA/IucC indicates aerobactin-family siderophore biosynthesis proteins, DesD indicates desferrioxamine siderophore synthetase, MbtG indicates a flavin-dependent lysine N6-monooxygenase involved in siderophore precursor biosynthesis, THNS indicates tetrahydroxynaphthalene synthase, and PKS indicates polyketide synthase.

Structural support for high-confidence core biosynthetic genes predicted by antiSMASH

Following antiSMASH-based genome mining, a subset of high-confidence core biosynthetic genes was selected for structural analysis to further support the genome-based functional annotation (Table 3). Gene selection was restricted to the biosynthetic enzymes with clearly assigned functions and suitable structural templates, resulting in six core enzymes derived from siderophore-, polyketide-, and terpene-associated biosynthetic gene clusters.

Homology modelling revealed conserved structural folds and catalytic domain organization among the predicted biosynthetic proteins and the experimentally characterized enzyme templates (Figure 5, Table 6). The siderophore-associated proteins from regions 4.1 and 7.1 displayed structural features characteristic of hydroxamate siderophore biosynthesis enzymes, including conserved monooxygenase and siderophore synthetase-like architectures. Similarly, proteins associated with terpene biosynthesis from region 10.2 expressed conserved prenyltransferase and cyclase-like folds linked to hopanoid and polyisoprenoid biosynthesis. In addition, the predicted type I and type III PKSs retained a characteristic modular and catalytic organization commonly observed in the bacterial polyketide biosynthetic enzymes. These structural similarities support the predicted biosynthetic roles of the selected proteins while avoiding direct inference of the enzymatic activity or the metabolite production.

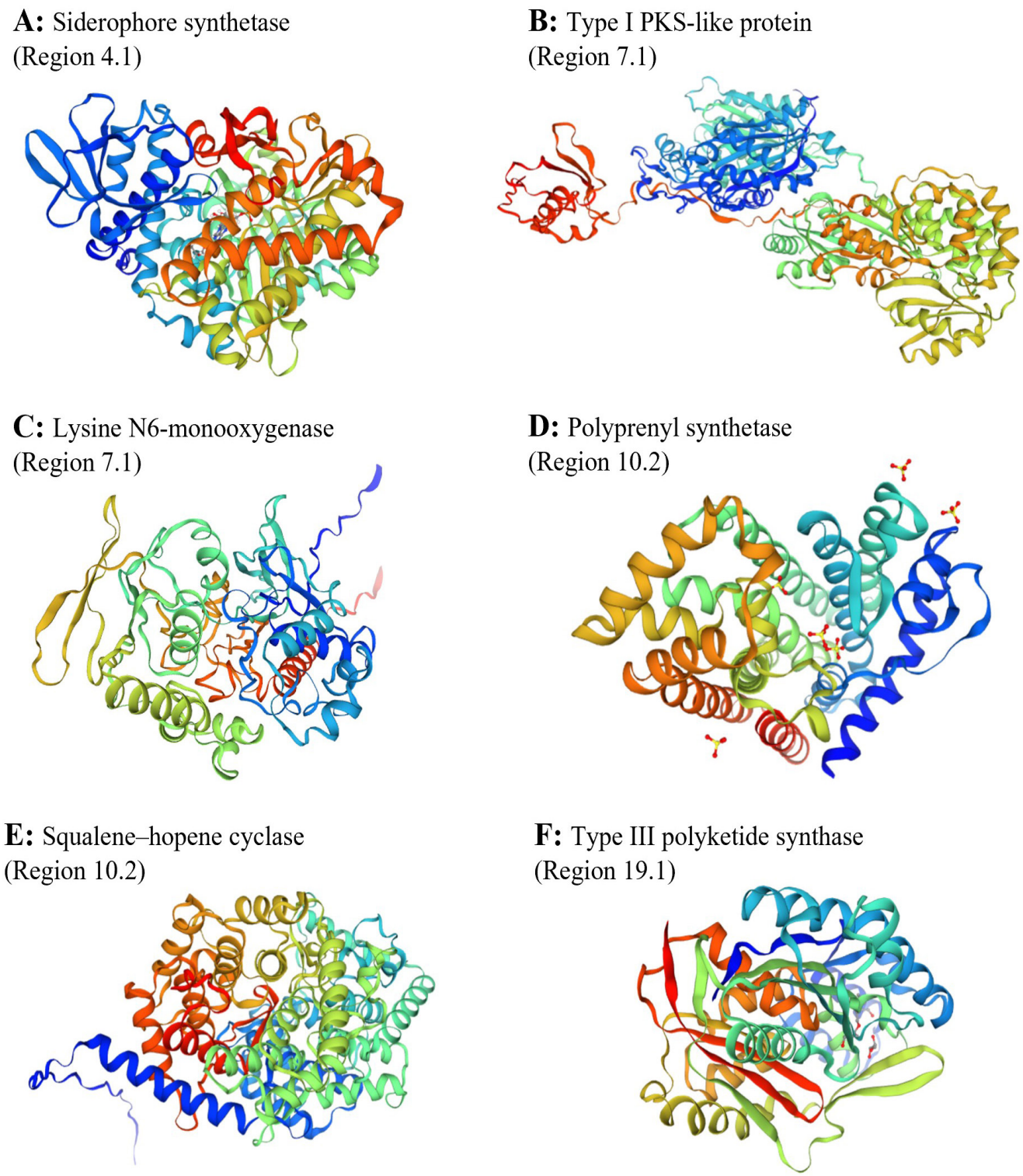

Figure 5: *Homology models of selected core biosynthetic proteins predicted from biosynthetic gene clusters in Streptomyces sp. S.PB5. Structural models were generated using SWISS-MODEL based on experimentally characterized protein templates. (A) Siderophore synthetase from region 4.1, (B) type I polyketide synthase-like protein from region 7.1, (C) lysine N6-monooxygenase from region 7.1, (D) polyprenyl synthetase from region 10.2, (E) squalene–hopene cyclase from region 10.2, and (F) type III polyketide synthase from region 19.1. The predicted proteins exhibited conserved structural folds and catalytic domain organization in consistency with known biosynthetic enzymes associated with siderophore, terpene, and polyketide biosynthesis. Structural modelling was used to support functional annotation and does not imply confirmed enzymatic activity or metabolite production.*

Discussion

This study examined the genomic characteristics that may underlie the plant growth–promoting and antagonistic activities previously reported for *Streptomyces* sp. isolate S.PB5 (Pengproh *et al.*, 2023). The genome of isolate S.PB5 was large, GC-rich, and encoded a substantial number of predicted protein-coding genes, a genomic profile typical of soil-inhabiting members of the genus *Streptomyces*. Genome-based phylogenetic reconstruction placed isolate S.PB5 within the *Streptomyces* clade but clearly separated it from the recognized type strains. This distinction was supported by the genome relatedness indices, as the highest digital DNA–DNA hybridization value (dDDH, formula d4) relative to the nearest reference strain *Streptomyces aquilus* GGCR-6 was 33.0%, which was well below the 70% species delineation threshold, while the maximum average nucleotide identity (88.69%) was also far below the commonly accepted 95–96% cutoff (Richter and Rosselló-Móra, 2009; Chun *et al.*, 2018; Meier-Kolthoff and Göker, 2019). Together, these metrics indicated that isolate S.PB5 represented a distinct genomic lineage within the genus rather than a member of an established species. Comparable genome sizes and GC-rich genomic architectures have been reported in other soil- and plant-associated *Streptomyces* species, supporting the view that large, GC-rich genomes are characteristic of the metabolically versatile actinobacteria adapted to the complex soil environments (Ashraf *et al.*, 2022; Borba *et al.*, 2023; Mechri *et al.*, 2025). In this context, the genomic features observed in isolate S.PB5 are consistent with the broad metabolic capacity and biosynthetic diversity commonly associated with the environmentally adapted *Streptomyces* isolates.

Functional annotation revealed that a substantial fraction of the isolate S.PB5 genome was assigned to pathways related to the central metabolism, nutrient acquisition, and stress response, a functional profile commonly reported for the soil- and the rhizosphere-associated bacteria exposed to a spatially and temporally variable resource availability. Genes associated with stress tolerance and detoxification were also identified, suggesting that genomic traits may contribute to the persistence under fluctuating soil conditions, although their activity and relevance *in situ* remain uncertain. Genome mining further identified a diverse complement of biosynthetic gene clusters, including NRPS, PKS, hybrid NRPS–PKS, terpene, siderophore, and RiPP-associated clusters. Several of these clusters showed similarity to the pathways involved in the biosynthesis of certain compounds such as ε-poly-L-lysine, desferrioxamine, coelichelin, albaflavenone, and aurantimycin A, which have been reported in other systems to possess an antimicrobial activity (Komaki *et al.*, 2020; Liu *et al.*, 2022; Mechri *et al.*, 2025). The presence of multiple biosynthetic pathways in the isolate S.PB5 genome is consistent with earlier observations of its antagonistic activity against *Fusarium oxysporum*; however, the expression, regulation, and functional contribution of these clusters under agricultural conditions remain to be determined.

Analysis of antiSMASH output revealed several biosynthetic gene clusters in isolate S.PB5 showing 100% similarity to the characterized reference clusters, including those associated with ectoine (region 1.2), geosmin (region 2.4), ε-poly-L-lysine (region 3.1), coelichelin (region 7.1), albaflavenone (region 14.2), informatipeptin (region 15.1), and the type III polyketide precursor 1,3,6,8-tetrahydroxynaphthalene (flaviolin; region 19.1), as summarized in Table 3. The presence of these conserved clusters indicated the genomic potential of isolate S.PB5 to produce diverse classes of secondary metabolites commonly associated with *Streptomyces* species, although experimental validation was required to confirm the metabolite production (Rutledge and Challis, 2015; Bentley *et al.*, 2002). In particular, siderophore-associated clusters identified in regions 4.1 and 7.1 suggested the potential for efficient iron acquisition, a trait that may provide a competitive advantage under iron-limited soil conditions and facilitate persistence in complex microbial communities (Ahmed and Holmström, 2014; Saha *et al.*, 2016). Siderophore-mediated iron sequestration has been reported to influence microbial interactions and pathogen suppression in other plant-associated systems (Siddiqui, 2006; Gu *et al.*, 2020), although the ecological and functional significance of these pathways in isolate S.PB5 warrants further functional investigation.

The genome of isolate S.PB5 contained genes associated with tryptophan-dependent auxin biosynthesis, nitrogen metabolism, urea degradation, phosphate metabolism, and inorganic phosphate transport, supporting its potential for nutrient transformation and plant-associated interactions. These genomic features

are consistent with the previously observed plant growth–promoting phenotypes of isolate S.PB5, including phosphate solubilization and siderophore production. In addition to the ecological functions, certain siderophore systems such as desferrioxamine B have also been implicated in iron homeostasis and developmental regulation in *Streptomyces* species (Codd *et al*., 2018). Therefore, the siderophore-associated clusters identified in isolate S.PB5 may have roles beyond iron acquisition, although their specific biological functions require experimental validation. However, the regulation and functional significance of these pathways under agricultural conditions have not yet been experimentally confirmed.

Soil environments are characterized by a fluctuating nutrient availability and intense microbial competition, conditions that are thought to favor metabolically versatile actinobacteria such as *Streptomyces* species (Krysenko and Wohlleben, 2024). In this context, the broad metabolic repertoire and regulatory functions observed in the isolate S.PB5 genome may contribute to the environmental persistence and the adaptive responses under nutrient-variable soil conditions. Genes associated with phosphate and nitrogen metabolism, transport systems, and stress response pathways are consistent with the physiological and the regulatory mechanisms previously reported in the soil-dwelling *Streptomyces* species, including PhoR/PhoP-associated nutrient regulation (Karandikar *et al*., 1997; Millan-Oropeza *et al*., 2020). The coexistence of these nutrient acquisition, transport, and stress response systems suggested a coordinated adaptive strategy that may enhance ecological competitiveness under fluctuating soil conditions. Efficient phosphate and nitrogen utilization may improve resource acquisition in nutrient-limited environments, while transport systems facilitate the uptake and redistribution of essential metabolites. Concurrently, stress response pathways may increase tolerance to environmental fluctuations, thereby supporting long-term survival and persistence (Karandikar *et al*., 1997; Millan-Oropeza *et al*., 2020). Together, these traits could promote niche adaptation by enabling S.PB5 to efficiently exploit available resources, respond to environmental stress, and maintain interactions within complex microbial communities and plant-associated habitats (Krysenko and Wohlleben, 2024).

Isolation of *Streptomyces* isolate S.PB5 from the cultivated soil associated with the extinct volcanic areas may also provide an ecological context for its broad metabolic and biosynthetic potentials. Volcanic-derived soils represent unique ecological habitats that support diverse microbial communities and may promote the persistence of metabolically versatile microorganisms adapted to dynamic environmental conditions (Gómez-Alvarez *et al*., 2007). In this context, the diverse biosynthetic gene clusters, extensive regulatory capacity, and nutrient-associated pathways currently identified in *Streptomyces* isolate S.PB5 are consistent with the ecological traits potentially advantageous for persistence and interaction within the complex soil environments. Nevertheless, several limitations should be acknowledged. The present study was based on a draft genome assembly generated from short-read sequencing data, which may not fully resolve the repetitive genomic regions or capture the complete architecture of all the biosynthetic gene clusters. Furthermore, the functional roles of the predicted genes and the biosynthetic pathways were inferred primarily through bio-informatic analyses and therefore require experimental validation. Although the specific contribution of the volcanic-associated environmental factors to the evolution and activity of *Streptomyces* isolate S.PB5 remains unclear, the present findings highlight the potential of the underexplored volcanic-associated soils as reservoirs of the genomically distinct and the functionally diverse *Streptomyces* strains.

Conclusions and Recommendations

This study provides genome-level insights into the plant growth–promoting and the antagonistic potential of *Streptomyces* sp. S.PB5, a strain previously isolated from cultivated soil associated with extinct volcanic areas in northeastern Thailand. Phylogenomic analyses demonstrated that *Streptomyces* isolate S.PB5 represents a distinct genomic lineage within the genus *Streptomyces*, supported by low ANI and dDDH values relative to the recognized reference strains. Genome mining and functional annotation revealed extensive biosynthetic and metabolic potentials, including diverse biosynthetic gene clusters associated with siderophores, polyketides, terpenes, RiPPs, and nutrient-related pathways linked to the plant-associated interactions. The genomic features identified in *Streptomyces* isolate S.PB5 are consistent with its previously reported plant growth–promoting and antagonistic phenotypes and suggest

substantial ecological adaptability in the complex soil environments. Although experimental validation of metabolite production and gene function remains necessary, the present findings highlight the potential of the volcanic-associated soils as reservoirs of genomically distinct and functionally diverse *Streptomyces* strains, with possible applications in sustainable agriculture and microbial biotechnology.

Future studies should incorporate transcriptomic, metabolomic, and greenhouse-based experiments to verify the functional expression and biological activities of the identified biosynthetic pathways. In addition, characterization of the metabolites produced by *Streptomyces* isolate S.PB5 and evaluation of its efficacy under greenhouse and field conditions will be imperative to assess its potential for agricultural and biotechnological applications.

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Novelty Statement

This study provides a genome mining–based characterization of *Streptomyces* sp. S.PB5 isolated from cultivated soils associated with extinct volcanic areas in northeastern Thailand, an underexplored ecological environment for agriculturally relevant actinobacteria. Unlike the previous studies that focused primarily on phenotypic characterization, this work integrates whole-genome annotation, phylogenomic analysis, biosynthetic gene cluster prediction, and in silico structural modelling to investigate the multifunctional genomic potential of this *Streptomyces* isolate S.PB5. The obtained results demonstrated that *Streptomyces* isolate S.PB5 represented a distinct genomic lineage within the genus *Streptomyces* and harbored diverse biosynthetic and nutrient-associated pathways linked to plant-associated interactions and antagonistic potential. These findings expand the current understanding of the genomic basis underlying plant growth promotion and secondary metabolism in environmentally adapted *Streptomyces* strains and provide a genomic framework for future functional validation and sustainable agricultural applications.

Authors Contribution

KS: Conceptualization, methodology, resources, supervision, writing–original draft
PK: Investigation, data curation, formal analysis, visualization, writing–original draft
TT: Formal analysis, writing–review and editing
RP: Investigation, data curation, formal analysis,
KhS: Formal analysis, writing–review and editing,
AS: Conceptualization, methodology, supervision, validation, writing–review and editing.
All authors have read and agreed to the published version of the manuscript.

Ethical approval
Ethical approval is not required for this study as it is purely computational and does not involve human subjects, animals, or live plants.

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Generative AI and AI assisted technology statement
The authors declare that no generative AI and AI assisted technology was used in the creation of this manuscript.

Conflict of interests
The authors have declared no conflicts of interest.

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